In the claims:

Please amend the claims as follows:

Claims 1 to 5 are withdrawn.

6. (currently amended) A method ~~of providing an array of proteins, the method~~ comprising:

providing a substrate with a plurality of addresses; and

providing at each address at least (i) a nucleic acid encoding an amino acid sequence comprising a test amino acid sequence and an affinity tag, and (ii) a binding agent that recognizes the affinity tag.

7. (currently amended) A method ~~of providing an array of proteins, the method~~ comprising:

providing a substrate with a plurality of addresses, each address comprising (i) a nucleic acid encoding ~~an~~ a hybrid amino acid sequence comprising a test amino acid sequence and an affinity tag, and (ii) a binding agent that recognizes the affinity tag;

contacting each address of the plurality with a translation effector to thereby translate the hybrid amino acid sequence; and

maintaining the substrate under conditions permissive for the hybrid amino acid sequence to bind the binding agent.

Claims 8 and 9 are withdrawn.

10. (currently amended) A method ~~of producing a protein interaction map for a plurality of amino acid sequences, the method~~ comprising:

providing (i) a first plurality of nucleic acids, each encoding an amino acid sequence comprising ~~an~~ a test amino acid sequence ~~of the plurality of amino acid sequences~~ and an affinity tag; (ii) a second plurality of nucleic acids, each encoding an amino acid sequence comprising ~~an~~ a test amino acid sequence ~~of the plurality of amino acid sequences~~ and a recognition tag; and

(iii) a substrate with a plurality of addresses and a binding agent that binds the affinity tag and is attached to the substrate; and

disposing on the substrate, at each address, a nucleic acid of the first plurality and a nucleic acid of the second plurality~~;~~

~~contacting each address of the plurality with a translation effector to thereby translate the hybrid amino acid sequence;~~

~~maintaining the substrate under conditions permissive for the affinity tag to bind binding agent;~~

~~washing the substrate to remove the translation extract and unbound polypeptides; and~~

~~detecting the recognition tag at each of the plurality of addresses~~.

11. (currently amended) A method comprising:

providing a substrate ~~comprising a providing a substrate~~ comprising a plurality of addresses, each address of the plurality having a binding agent;

providing a plurality of nucleic acid sequences, each nucleic acid sequence comprising a sequence encoding a test amino acid sequence and an affinity tag that is recognized by the binding agent;

~~providing on a server a list of either (i) nucleic acid sequences of the plurality or (ii) subsets of the plurality~~;

transmitting, from a server, one or more choices for amino acids to include on the substrate ~~the list~~ across a network to a user;

receiving at least one selection ~~of the list~~ from the user; and

disposing the one or more nucleic acid sequence corresponding to the selection on an address of the plurality~~; and~~

~~providing the substrate to the user~~.

12. (new) The method of claim 6 further comprising contacting each address of the plurality with a transcription effector.

13. (new) The method of claim 6 further comprising contacting each address of the plurality with a translation effector.

14. (new) The method of claim 6 further comprising contacting each address of the plurality with a transcription effector and a translation effector.

15. (new) The method of claim 13 wherein the translation effector comprises a translation extract prepared from cells.

16. (new) The method of claim 13 further comprising contacting each address of the plurality with a chaperone.

17. (new) The method of claim 6 further comprising enclosing the substrate in an air- or water- resistant package.

18. (new) The method of claim 6 wherein each test amino acid sequence is unique.

19. (new) The method of claim 6 wherein the affinity tag is separated from the test amino acid sequence by at least five amino acids.

20. (new) The method of claim 6 wherein the affinity tag encoded by the nucleic acid at each address of the plurality is the same.

21. (new) The method of claim 6 wherein the affinity tag encoded by the nucleic acid at an address of the plurality differs from at least one other affinity tag in the plurality of addresses.

22. (new) The method of claim 6 wherein the nucleic acid is DNA.

23. (new) The method of claim 22 wherein the nucleic acid is double stranded DNA.

24. (new) The method of claim 22 wherein the nucleic acid comprises an operably linked transcription promoter.

25. (new) The method of claim 6 wherein the nucleic acid comprises an internal ribosome entry site.

26. (new) The method of claim 6 wherein the nucleic acid comprises a plurality of cistrons.

27. (new) The method of claim 6 wherein the nucleic acid comprises a sequence that encodes a reporter protein.

28. (new) The method of claim 27 wherein the reporter protein can produce or modulate light.

29. (new) The method of claim 6 wherein the transcription promoter is a prokaryotic promoter.

30. (new) The method of claim 6 wherein the amino acid sequence comprises an intein.

31. (new) The method of claim 6 wherein the substrate is partitioned.

32. (new) The method of claim 6 wherein the substrate comprises at least 1 address per $cm^2$.

33. (new) The method of claim 32 wherein the substrate comprises at least 10 addresses per $cm^2$.

34. (new) The method of claim 6 wherein each address contains less than 1 ng of the nucleic acid.

35. (new) The method of claim 6 wherein each address contains less than 10 pg of the nucleic acid.

36. (new) The method of claim 6 wherein the binding agent comprises a biological polymer.

37. (new) The method of claim 6 wherein the binding agent is covalently attached to the substrate.

38. (new) The method of claim 6 wherein the binding agent is attached by a bridging moiety.

39. (new) The method of claim 6 wherein the binding agent is an antibody.

40. (new) The method of claim 6 wherein affinity tag comprises a polypeptide sequence which can chelate metal.

41. (new) The method of claim 40 wherein affinity tag comprises hexa-histidine.

42. (new) The method of claim 6 wherein affinity tag comprises a protein selected from the group consisting of glutathione-S-transferase, chitin binding protein, cellulase, maltose binding protein, dihydrofolate reductase, and FK506 binding protein (FKBP).

43. (new) The method of claim 13 further comprising contacting each address of the plurality with a protein-modifying enzyme.

44. (new) The method of claim 6 wherein the nucleic acid comprises a site-specific recombination site.

45. (new) The method of claim 6 wherein each address comprises a plurality of nucleic acid sequences, each encoding a unique test amino acid sequence and an affinity tag.

46. (new) The method of claim 6 wherein the providing comprises mechanically delivering the nucleic acid to each address of the plurality of addresses.

47. (new) The method of claim 6 wherein the providing comprises amplifying a template nucleic acid to provide a nucleic acid for each address of the plurality of addresses.

48. (new) The method of claim 7 further comprising contacting cells to the substrate and evaluating the cells or a parameter of the cells.

49. (new) The method of claim 7 further comprising contacting members of a display library to the substrate.

50. (new) The method of claim 7 further comprising contacting a patient sample to the substrate.

51. (new) The method of claim 50 further comprising further comprising detecting binding of the patient sample to the array.

52. (new) The method of claim 51 further comprising recording results of the detecting in a database.

53. (new) The method of claim 7 wherein the test amino acid sequences at the plurality of addresses comprise allergens and/or auto-immune antigens.

54. (new) The method of claim 7 wherein the test amino acid sequences at the plurality of addresses comprise naturally occurring sequences.

55. (new) The method of claim 54 wherein the test amino acid sequences at the plurality of addresses comprise bacterial antigens.

56. (new) The method of claim 54 wherein the test amino acid sequences at the plurality of addresses comprise viral antigens.

57. (new) The method of claim 56 wherein the viral antigens comprise antigens from a rotavirus, hepatitis virus, herpes virus, papilloma virus and/or a retrovirus.

58. (new) The method of claim 7 wherein the test amino acid sequences at the plurality of addresses comprise artificial amino acid sequences.

59. (new) The method of claim 7 wherein the test amino acid sequences at the plurality of addresses comprise transmembrane proteins whose transmembrane domains have been excised.

60. (new) The method of claim 7 wherein the test amino acid sequences at the plurality of addresses comprise randomized amino acid sequences.

61. (new) The method of claim 7 wherein the test amino acid sequence comprises an immunoglobulin variable domain.

62. (new) The method of claim 7 further comprising contacting endoplasmic reticulum vesicles to the array.

63. (new) The method of claim 7 wherein the substrate comprises at least 10 addresses per $cm^2$.

64. (new) The method of claim 7 wherein each address contains less than 1 ng of the nucleic acid.

65. (new) The method of claim 7 wherein each address contains less than 10 pg of the nucleic acid.

66. (new) The method of claim 22 wherein the DNA comprises plasmid DNA.

67. (new) The method of claim 22 wherein the DNA comprises a PCR product.

68. (new) The method of claim 6 wherein the providing of nucleic acid at each address comprise:

providing a collection of nucleic acids, each member of the collection being compatible with a recombinational cloning system and including an open reading frame of interest;

recombining members of the collection with a recipient nucleic acid that comprises a nucleic acid sequence encoding an affinity tag such that the open reading frame is linked in frame to the nucleic acid sequence encoding the affinity tag; and

disposing nucleic acid derived from the recombination at addresses of the plurality of addresses.

69. (new) The method of claim 68 wherein the collection comprises at least 500 members.

70. (new) The method of claim 68 wherein members of the collection are identified by a locator accessible to a robotic system.

71. (new) The method of claim 68 wherein members of the collection are referenced by a relational database that includes information about storage location and a link to another biological database.

72. (new) The method of claim 7 wherein each address further comprises a nucleic acid encoding a modifying enzyme.

73. (new) The method of claim 72 wherein the modifying enzyme is varied among the addresses of the plurality.

74. (new) The method of claim 10 further comprising:

contacting each address of the plurality with a translation effector to thereby translate the nucleic acid of the first plurality and the nucleic acid of the second plurality; and

maintaining the substrate under conditions permissive for the affinity tag to bind the binding agent.

75. (new) The method of claim 74 further comprising washing the substrate to remove the translation extract and unbound polypeptides.

76. (new) The method of claim 75 further comprising detecting the recognition tag at addresses of the plurality of addresses.

77. (new) The method of claim 10 wherein the recognition tag comprises an epitope tag, an enzyme, or a fluorescent protein.

78. (new) The method of claim 11 further comprising providing the substrate to the user.

79. (new) The method of claim 11 wherein the server is interfaced with a robotic system, and the at least one selection is communicated from the server to the robotic system.

80. (new) The method of claim 11 wherein the choices are arranged hierarchically.

81. (new) The method of claim 11 wherein the choices comprise a list of general user needs.

82. (new) The method of claim 11 wherein the choices comprise a list of classes of amino acid sequences.

83. (new) The method of claim 11 wherein the choices comprise individual amino acid sequences.

84. (new) The method of claim 82 wherein the classes comprise entries correlated with a condition or disease.

85. (new) The method of claim 82 wherein the classes comprise entries correlated with a protein family.

86. (new) The method of claim 82 wherein the classes comprise entries correlated with an organismal species.

87. (new) The method of claim 11 wherein the server recommends a control amino acid sequence based on user selections.

88. (new) The method of claim 7 further comprising evaluating the substrate for a fluorescence.

89. (new) The method of claim 7 further comprising evaluating the substrate using mass spectroscopy.

90. (new) The method of claim 7 further comprising evaluating the substrate for a fluorescent property.

91. (new) The method of claim 7 further comprising evaluating the substrate for an enzymatic property.

92. (new) The method of claim 7 further comprising evaluating the plurality of addresses on the substrate, and recording results of the evaluating in records of a database.

93. (new) The method of claim 92 further comprising clustering the records to identify addresses which are related.

94. (new) The method of claim 92 further comprising making results of the evaluating accessible to a network of health care providers.

95. (new) The method of claim 92 further comprising making results of the evaluating accessible to a physician.